RAW SEQUENCE LISTING

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Application Serial Number: _09/234,208E_

Source: _/Fw/6_

Date Processed by STIC: _8/29/05_

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RAW SEQUENCE LISTING   DATE: 08/29/2005
PATENT APPLICATION: **US/09/234,208E**   TIME: 14:55:57

Input Set : **A:\49321-1 SEQ LIST.txt**
Output Set: **N:\CRF4\08292005\I234208E.raw**

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 3 <110> APPLICANT: Doherty, Joni Kristin
 4         Clinton, Gail M.
 6 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
 8 <130> FILE REFERENCE: 49321-1
10 <140> CURRENT APPLICATION NUMBER: 09/234,208E
11 <141> CURRENT FILING DATE: 1999-01-20
13 <160> NUMBER OF SEQ ID NOS: 12
15 <170> SOFTWARE: PatentIn version 3.3
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 79
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
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28 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
29              20                  25                  30
32 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
33          35                  40                  45
36 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
37      50                  55                  60
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41 65                  70                  75
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45 <211> LENGTH: 419
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
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56              20                  25                  30
59 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
60          35                  40                  45
63 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
64      50                  55                  60
67 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
68 65                  70                  75                  80
71 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
72              85                  90                  95
75 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
76              100                 105                 110
79 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
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80        115                 120                 125
83 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
84        130                 135                 140
87 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
88 145                 150                 155                 160
91 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
92                 165                 170                 175
95 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
96                 180                 185                 190
99 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
100                 195                 200                 205
103 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
104        210                 215                 220
107 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
108 225                 230                 235                 240
111 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
112                 245                 250                 255
115 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
116                 260                 265                 270
119 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
120                 275                 280                 285
123 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
124        290                 295                 300
127 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
128 305                 310                 315                 320
131 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
132                 325                 330                 335
135 Pro Cys Ala Arg Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val
136        340                 345                 350
139 Pro Val Pro Leu Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser
140        355                 360                 365
143 Phe Leu Arg Pro Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro
144        370                 375                 380
147 Leu Ala Pro Leu Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val
148 385                 390                 395                 400
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152                 405                 410                 415
155 Tyr Glu Gly
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 19
161 <212> TYPE: DNA
162 <213> ORGANISM: artificial sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: primer
167 <400> SEQUENCE: 3
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172 <211> LENGTH: 22
173 <212> TYPE: DNA
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174 <213> ORGANISM: artificial sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: primer
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186 <213> ORGANISM: artificial sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: primer
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196 <211> LENGTH: 21
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198 <213> ORGANISM: artificial sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 6
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208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: artificial sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: primer
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219 <210> SEQ ID NO: 8
220 <211> LENGTH: 22
221 <212> TYPE: DNA
222 <213> ORGANISM: artificial sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: primer
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231 <210> SEQ ID NO: 9
232 <211> LENGTH: 27
233 <212> TYPE: DNA
234 <213> ORGANISM: artificial sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: primer
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240 gcacggatcc atagcagact gaggagg                                     27
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244 <211> LENGTH: 287
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING   DATE: 08/29/2005
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Input Set : **A:\49321-1 SEQ LIST.txt**
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248 <400> SEQUENCE: 10
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251 agcctggccc agcccaccct gtcctatcct tcctcagacc ctcttgggac ctagtctctg   120
253 ccttctactc tctacccctg gcccccctca gccccacaag tgtccctata tccccctgtca   180
255 gtgtggggag gggcccggac cctgatgctc atgtggctgt taacctgtcc cggtatgaag   240
257 gctgagacgg cccctctccc cacccacccc cacctcctca gtgtgct                 287
260 <210> SEQ ID NO: 11
261 <211> LENGTH: 276
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapiens
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(240)
269 <223> OTHER INFORMATION: ECDIIIa intron-encoded region of herstatin
271 <400> SEQUENCE: 11
272 ggt acc cac tca ctg ctc ccg agg cca gct gca gtt cct gtc cct ctg    48
273 Gly Thr His Ser Leu Leu Pro Arg Pro Ala Ala Val Pro Val Pro Leu
274 1               5                  10                  15
276 cgc atg cag cct ggc cca gcc cac cct gtc cta tcc ttc ctc aga ccc    96
277 Arg Met Gln Pro Gly Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
278             20                  25                  30
280 tct tgg gac cta gtc tct gcc ttc tac tct cta ccc ctg gcc ccc ctc   144
281 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
282         35                  40                  45
284 agc ccc aca agt gtc cct ata tcc cct gtc agt gtg ggg agg ggc ccg   192
285 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
286     50                  55                  60
288 gac cct gat gct cat gtg gct gtt aac ctg tcc cgg tat gaa ggc tga   240
289 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly
290 65                  70                  75
292 gacggcccct tcccccaccc accccacct cctcag                             276
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296 <211> LENGTH: 79
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 12
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307             20                  25                  30
310 Ser Trp Asp Leu Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
311         35                  40                  45
314 Ser Pro Thr Ser Val Pro Ile Ser Pro Val Ser Val Gly Arg Gly Pro
315     50                  55                  60
318 Asp Pro Asp Ala His Val Ala Val Asn Leu Ser Arg Tyr Glu Gly
319 65                  70                  75
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VERIFICATION SUMMARY   DATE: 08/29/2005
PATENT APPLICATION: **US/09/234,208E**   TIME: 14:55:58

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